

G437S — WFS1 Molecular Atlas Card

Variant type: Missense

Substitution: Glycine (G) → Serine (S) at position 437

Domain context: Transmembrane helix 5

ALPHAMISSENSE

- **Pathogenicity score:** 0.0824
- **Class:** likely benign

ALPHAFOLD CONFIDENCE

- **pLDDT at residue 437:** 90.31

> **DynaMut2 $\Delta\Delta G$:** not yet computed for this variant — AlphaMissense + AlphaFold

> confidence shown above. Stability $\Delta\Delta G$ and the wild-type/mutant structural

> comparison backfill behind this note.

CLINICAL EVIDENCE

- **Classification:** Benign/Likely benign
 - **Review status:** criteria provided, multiple submitters, no conflicts
 - **Associated conditions:** WFS1-Related Spectrum Disorders; Autosomal dominant nonsyndromic hearing loss 6
 - **cDNA change:** c.1309G>A
 - **ClinVar accession:** VCV000215356
 - **Last evaluated:** 2026/03/13 00:00
 - **Submissions:** 1
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Card generated by `wolfram-atlas-batch` (missense AlphaMissense mint) on 2026-06-08T02:27:33.533112Z.

AlphaMissense (Cheng et al. 2023) · AlphaFold model v6 · UniProt O76024.